

Fig. 1A

GAGCTTCTG GGGAGTGAGG GAAGCGGTTT ACAGTGAAT TGGTGGAGC CTCAGGGGGC GGAAGTGGCA CGGAACACAC  
 CCGTAGGCCA GCCTGGGTG CCAGGCGGA GCTGCTCTT CTCCGCGGG TTGGTGACC CGCTCAGTAC GGAGTGGGG  
 AAGCTCTTC ACTTCGGAGG ATTGCTCAAC AACC 194  
 ATG CTG GGC ATC TGG ACC CTC CTA CCT CTG GTT CTT ACG TCT GTT GCT AGA TTA TCG TCC AAA AGT  
 Met Leu Gly Ile Trp Thr Leu Leu Pro Leu Val Leu Thr Ser Val Ala Arg Leu Ser Ser Lys Ser  
 -10 -1 1  
 GTT AAT GCC CAA GTG ACT GAC ATC AAC TCC AAG GGA TTG GAA TTG AGG AAG ACT GTT ACT ACA GTT  
 Val Asn Ala Gln Val Thr Asp Ile Asn Ser Lys Gly Leu Glu Leu Arg Lys Thr Val Thr Thr Val  
 10 20  
 GAG ACT CAG AAC TTG GAA GGC CTG CAT CAT GAT GGC CAA TTC TGC CAT AAG CCC TGT CCT CCA GGT  
 Glu Thr Gln Asn Leu Glu Gly Leu His His Asp Gly Gln Phe Cys His Lys Pro Cys Pro Pro Gly  
 30 40 50  
 GAA AGG AAA GCT AGG GAC TGC ACA GTC AAT GGG GAT GAA CCA GAC TGC GTG CCC TGC CAA GAA GGG  
 Glu Arg Lys Ala Arg Asp Cys Thr Val Asn Gly Asp Glu Pro Asp Cys Val Pro Cys Gln Glu Gly  
 60 70  
 AAG GAG TAC ACA GAC AAA GCC CAT TTT TCT TCC AAA TGC AGA TGT AGA TTG TGT GAT GAA GGA  
 Lys Glu Tyr Thr Asp Lys Ala His Phe Ser Ser Lys Cys Arg Arg Cys Arg Leu Cys Asp Glu Gly  
 80 90  
 CAT GGC TTA GAA GTG GAA ATA AAC TGC ACC CGG ACC CAG AAT ACC AAG TGC AGA TGT AAA CCA AAC  
 His Gly Leu Glu Val Glu Ile Asn Cys Thr Arg Thr Gln Asn Thr Lys Cys Arg Cys Lys Pro Asn  
 100 110  
 TTT TTT TGT AAC TCT ACT GTA TGT GAA CAC TGT GAC CCT TGC ACC AAA TGT GAA CAT GGA ATC ATC  
 Phe Phe Cys Asn Ser Thr Val Cys Glu His Cys Asp Pro Cys Thr Lys Cys Glu His Gly Ile Ile  
 \*120 \*130

Fig. 1B

AAG GAA TGC ACA CTC ACC AGC AAC ACC AAG TGC AAA GAG GAA GGA TCC AGA TCT AAC TTG GGG TGG	
Lys Glu Cys Thr Leu Thr Ser Asn Thr Lys Cys Lys Glu Glu Gly Ser Arg Ser Asn Leu Gly Trp	160
CTT TGT CTT CTT TTG CCA ATT CCA CTA ATT GTT TGG GTG AAG ACG AAG GAA GTA CAG AAA ACA	
Leu Cys Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys Thr	170
TGC AGA AAG CAC AGA AAG GAA AAC CAA GGT TCT CAT GAA TCT CCA ACC TTA AAT CCT GAA ACA GTG	
Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val	180
GCA ATA AAT TTA TCT GAT GTT GAC TTG AGT AAA TAT ATC ACC ACT ATT GCT GGA GTC ATG ACA CTA	
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Thr Ala Gly Val Met Thr Leu	190
AGT CAA GTT AAA GGC TTT GTT CGA AAG AAT GGT GTC AAT GAA GCC AAA ATA GAT GAG ATC ARG AAT	
Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn	200
GAC AAT GTC CAA GAC ACA GCA GAA CAG AAA GTT CAA CTG CTT CGT AAT TGG CAT CAA CTT CAT GGA	
Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly	210
AAG AAA GAA GCG TAT GAC ACA TTG ATT AAA GAT CTC AAA AAA	
Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys	220

Fig. 2A

1100  
GCC AAT CTT TGT ACT CTT GCA GAG AAA ATT CAG ACT ATC ATC CTC AAG GAC ATT ACT AGT GAC TCA  
Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser  
290 300 1150

GAA AAT TCA AAC TTC AGA AAT GAA ATC CAA AGC TTG GTC TAG ACTGAAAAACAACAAATTCAGTTCTGA  
Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val End  
310 1200

GTATATGCAATTAGTGTGTTGAAAAGATTCTTAATAGCTGGCTGTAATACCTGCTTGGTTTTTACTGGGTACATTTTATC  
1250 1300

ATTTATTAGCGGTGAAGAGCCACATATTTTGTAGATTTTAAATATCTCATGATTCTGCCTCCAAGGATGTTTAAATCTA  
1400 1450

GTTGGAAAAACAACCTTCATCAAGAGTAATGCAGTGGCAGCTAAGTACCCAAATAGGAGTGTGTCAGAGGATGAAAG  
1500 1550

ATTAAGATTATGCTCTGGCATCTAACATATGATTTCTGTAGTATGAATGTAATCAGTGTATGTTAGTACAAATGTTCTATCC  
1600 1650

ACAGGCTAACCCACTCTATGAATCAATAGAAGCTATGACCTTTTGCTGAAATATCAGTTACTGAACAGGCAGGCCA  
1700

CTTTGCCCTCAAAATACCTCTGATAAATCTAGAGATTTTACCATAATTTCTAAAACCTTTGTTTATAACTCTGAGAAGATCAT  
1750

ATTTATGTAAGTATATGTTAGTGCAAAATTAATAAGGCTACCTCAAGACCTTTGCACAGTTATTGGTGT  
-----

Fig. 2B

1800  
 CATATTACAATATTTCAATTGTGAATTCACATAGAAAACATTAATAATGTTTGACATTTATATATATGTGTATGCA  
 1850  
 TTTTACTGGCTCAAAACTACCTACTCTTTCTCAGGCATCAAAAGCATTGACAGGAGAGTATTACTAGAGCTTTGCC  
 1900  
 ACCTCTCCATTTTGGCTTGGTGTCTCATCTTAATGGCCTAATGCACCCCAACATGGAATATCACCAAAAATACTTTA  
 2000  
 ATAGTCCACCAAAAGGCAAGACTGCCCTTAGAAATCTAGCCTGGTTGGAGTACTAACTGCTCTCAGAGAAAAGTAGCT  
 2050  
 TTGTGACATGTGATGAACCATGTTTGCATCAAGATGATAAAATAGATCTTATTTTCCCCCACCCCGAAAAATGTT  
 2100  
 CAATAATGTCCTGATAAACCTGCTACAAATGCCAGCTTATACATAGCAATGGTAAATCATCTCGATTTTAGCAAT  
 2150  
 TGCTCTTCTCATACCCCTCAAGTTTCTAAGATTTAAGATTCTCCTTACCTACTATCCTAGCTTTAAATATCTTTGAAAGTTT  
 2200  
 GTATTAAATGTGAATTTAAGAAATAATATTATATTCTGTAAATGTAACCTGTGAAGATAGTTATAAACTGAAGCAGA  
 2250  
 TACCTGGAACCACTAAAGAACCTCCATTATGGAGGATTTTTTGGCCCTTGTGTGTGAATATAAAATATAGGTAAA  
 2300  
 2350  
 2400  
 2450  
 2500  
 AGTACGTAATTAAATAATGTTTTTG

FIG 3A

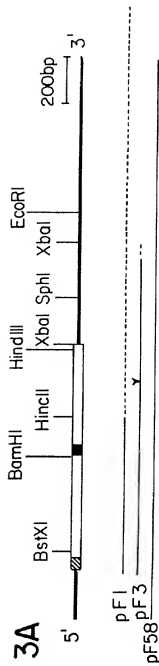


FIG 3B

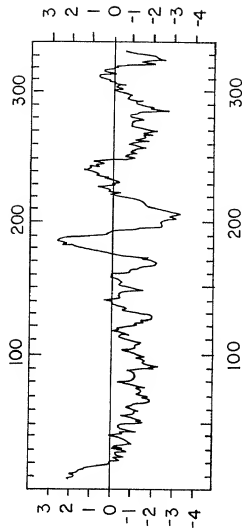


FIG.4A

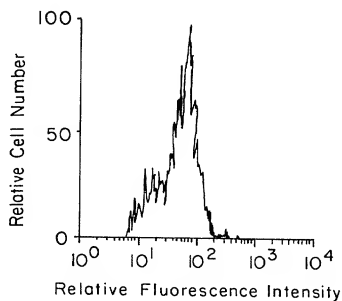


FIG.4B

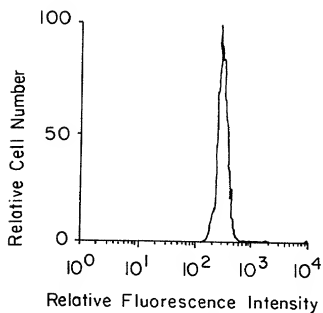


FIG. 4C

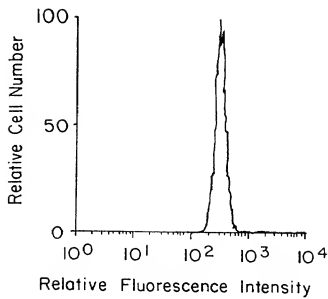


FIG. 4D

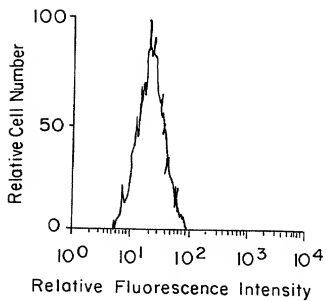


FIG. 4E

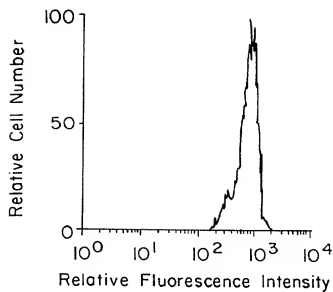


FIG. 4F

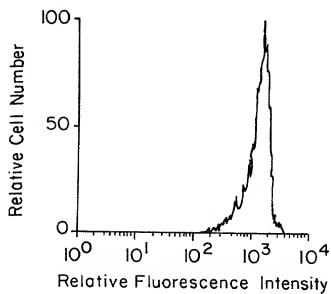




FIG. 5

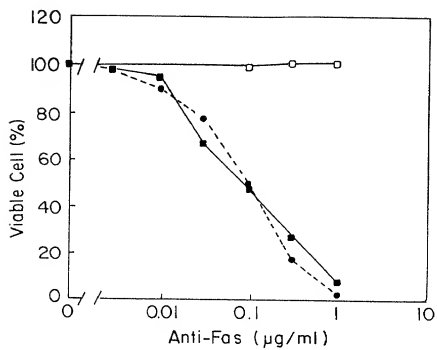


FIG. 6

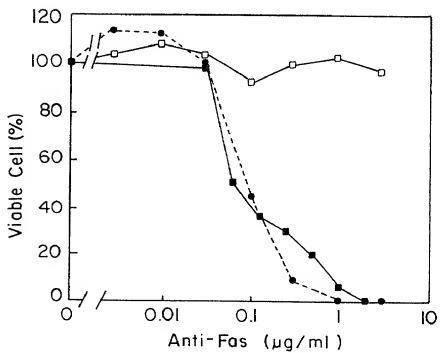
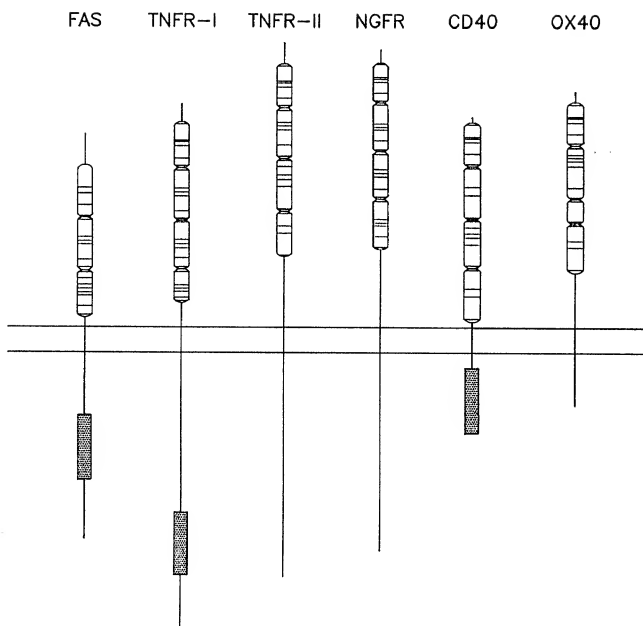


FIG.7



09884987.062101

**Fig. 8A**

	Q	N	L	E	G	H	I	D	G	Q	F	-	-	-	-	-	C	H	-	T	S	R	-
hFAS (31-67)	V	C	P	Q	G	L	Y	D	Q	N	A	-	-	-	-	-	C	C	-	-	-	-	-
hTNR1 (3-42)	T	C	R	L	R	E	Y	D	Q	N	A	-	-	-	-	-	C	C	-	-	-	-	-
hTNR2 (39-76)	A	C	P	T	G	L	Y	T	S	E	-	-	-	-	-	-	C	C	-	-	-	-	-
hNGFR (3-37)	A	C	P	T	G	L	Y	T	S	E	-	-	-	-	-	-	C	C	-	-	-	-	-
hCD40 (25-60)	A	C	R	E	K	Q	Y	I	N	S	Q	-	-	-	-	-	C	C	-	-	-	-	-
roX40 (29-60)	N	C	V	K	D	T	Y	S	G	H	K	-	-	-	-	-	C	C	-	-	-	-	-
hFAS (68-112)	P	C	Q	E	G	K	E	T	D	K	A	-	-	-	-	-	R	C	-	-	-	-	-
hTNR1 (43-86)	E	C	E	S	G	S	F	T	S	E	N	-	-	-	-	-	R	C	-	-	-	-	-
hTNR2 (77-119)	S	C	E	D	S	T	Y	Q	L	E	W	-	-	-	-	-	R	C	-	-	-	-	-
hNGFR (38-80)	P	C	L	D	S	V	T	S	D	V	S	-	-	-	-	-	C	C	-	-	-	-	-
hCD40 (61-104)	P	C	G	E	S	E	F	L	T	W	S	-	-	-	-	-	C	C	-	-	-	-	-
roX40 (61-103)	P	C	-	E	P	G	F	Y	E	A	N	-	-	-	-	-	C	C	-	-	-	-	-
hFAS (113-149)	-	C	K	P	N	F	F	N	-	-	S	-	-	-	-	-	C	C	-	-	-	-	-
hTNR1 (87-126)	-	C	R	K	N	Q	Y	H	Y	W	T	-	-	-	-	-	C	C	-	-	-	-	-
hTNR2 (120-162)	-	C	R	P	G	W	Y	A	-	-	E	-	-	-	-	-	C	C	-	-	-	-	-
hNGFR (81-119)	-	C	A	Y	G	Y	Y	Q	-	-	-	-	-	-	-	-	C	C	-	-	-	-	-
hCD40 (105-144)	-	C	E	E	G	W	H	C	-	-	-	-	-	-	-	-	C	C	-	-	-	-	-
roX40 (104-123)	-	C	R	P	G	T	Q	P	-	-	-	-	-	-	-	-	C	C	-	-	-	-	-
hTNR1 (127-155)	T	C	H	A	G	F	F	R	-	-	E	-	-	-	-	-	C	C	-	-	-	-	-
hTNR2 (163-201)	P	C	A	P	G	T	F	N	T	-	S	-	-	-	-	-	C	C	-	-	-	-	-
hNGFR (120-161)	E	C	P	D	G	T	Y	S	E	A	N	-	-	-	-	-	C	C	-	-	-	-	-
hCD40 (145-186)	P	C	P	V	G	F	F	S	N	V	S	-	-	-	-	-	C	C	-	-	-	-	-
roX40 (124-164)	P	C	P	P	G	H	F	S	S	G	N	-	-	-	-	-	C	C	-	-	-	-	-
Consensus	C	G	G	S	Y	F	S	S	P	G	Q	-	-	-	-	-	C	C	-	-	-	-	-



Fig 9

hCD40 (225-247)	K A P H P K Q E P Q E P I N F P D L P G S N T
hFAS (230-251)	K G F V R K N G V N E A K I - D E I K N D N V
hTNFRI (332-353)	K E F V R R L G S D H E I - D R L E L Q N G
hCD40 (248-269)	A A P V Q E T L H G C Q P V - Q E D G - K E S
hFAS (252-274)	Q D T A E Q K V Q L R N W W E L H G K E A
hTNFRI (354-376)	R C L R E A Q Y S L A T W R R P R R E A